9. (Twice amended) A method for detecting the presence of a polypeptide having an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence shown in SEQ ID NO:1; and

(b) the amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369;

said method comprising contacting said sample with an agent that specifically allows detection of the presence of the polypeptide in the sample and then detecting the presence of the polypeptide.

18. (Twice Amended) A method for identifying an agent that binds to a polypeptide having an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence shown in SEQ ID NO:1; and

(b) the amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369;

said method comprising contacting the polypeptide with an agent that binds to the polypeptide and assaying the complex formed with the agent bound to the polypeptide.

19. (Twice amended) A method for modulating the activity of a polypeptide having an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence shown in SEQ ID NO:1; and

(b) the amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369;

said method comprising contacting the polypeptide with an agent under conditions that allow the agent to modulate the activity of the polypeptide.

REMARKS

Claims 2, 9-14, 18-20, 22-30, and 33-37 are pending in the current application. Claims 2, 9, 18, and 19 have been amended to delete clauses (c), (d), (e), (f), (g), (h), (i), (j), (k), (l), and (m), directed to sequence variants and fragments. This subject matter is cancelled without

prejudice or disclaimer of the subject matter contained therein. Applicants expressly reserve the right to file continuation applications or take such other appropriate measures deemed necessary to protect the cancelled subject matter. The amendment reduces issues for appeal and thereby places the claim in better form for consideration on appeal. The amendment does not raise any new issues or require further consideration or search. Accordingly, entry of the amendment is respectfully requested.

CONCLUSIONS

It is not believed that extensions of time or fees for net addition of claims are required, beyond those, which may otherwise be provided for in documents accompanying this paper. However, in the event that additional extensions of time are necessary to allow consideration of this paper, such extensions are hereby petitioned under 37 CFR §1.136(a), and any fee required therefore (including fees for net addition of claims) is hereby authorized to be charged to Deposit Account No. 16-0605.

Respectfully submitted,

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CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to: **BOX AF**, Commissioner For Patents, Washington, DC 20231, on October 29, 2001.

Nora C. Martinez

Nora C. Martinez

Version with Markings to Show Changes Made:

In the Claims:

Please amend claims 2, 9, 18, and 19 as follows:

2. (Twice amended) An isolated antibody that selectively binds to a polypeptide having an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence shown in SEQ ID NO:1; and

(b) the amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369.[;

(c) the amino acid sequence of an allelic variant of the amino acid sequence shown in SEQ ID NO:1;

(d) the amino acid sequence of an allelic variant of the amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369;

(e) the amino acid sequence of a sequence variant of the amino acid sequence shown in SEQ ID NO:1, wherein the sequence variant is encoded by a nucleic acid molecule hybridizing to the nucleic acid molecule shown in SEQ ID NO 2 under stringent conditions;

(f) the amino acid sequence of a sequence variant of the amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. PTA-2369, wherein the sequence variant is encoded by a nucleic acid molecule hybridizing under stringent conditions to the cDNA contained in ATCC Deposit No. PTA-2369;

(g) a fragment of the amino acid sequence shown in SEQ ID NO:1, wherein the fragment comprises at least 12 contiguous amino acids;

(h) a fragment of the amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369, wherein the fragment comprises at least 12 contiguous amino acids;

(i) the amino acid sequence of the mature receptor polypeptide from about amino acid 6 to about amino acid 359, shown in SEQ ID NO:1;

(j) the amino acid sequence of the mature polypeptide from about amino acid 6 to about amino acid 359, encoded by the cDNA clone contained in ATCC Deposit No. PTA-2369;

(k) the amino acid sequence of the transmembrane domain of the polypeptide shown in SEQ ID NO:1, from about amino acid 43 to about amino acid 318;

(l) the amino acid sequence of the transmembrane domain from about amino acid 43 to about amino acid 318 in the polypeptide encoded by the cDNA contained in ATCC Deposit No. PTA-2369;

(m) the amino acid sequence of an epitope bearing region of any one of the polypeptides of (a)-(l).]

9. (Twice amended) A method for detecting the presence of a polypeptide having an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence shown in SEQ ID NO:1; and

(b) the amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369;

[(c) the amino acid sequence of an allelic variant of the amino acid sequence shown in SEQ ID NO:1;

(d) the amino acid sequence of an allelic variant of the amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369;

(e) the amino acid sequence of a sequence variant of the amino acid sequence shown in SEQ ID NO:1, wherein the sequence variant is encoded by a nucleic acid molecule hybridizing to the nucleic acid molecule shown in SEQ ID NO 2 under stringent conditions;

(f) the amino acid sequence of a sequence variant of the amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. PTA-2369, wherein the sequence variant is encoded by a nucleic acid molecule hybridizing under stringent conditions to the cDNA contained in ATCC Deposit No. PTA-2369;

(g) a fragment of the amino acid sequence shown in SEQ ID NO:1, wherein the fragment comprises at least 12 contiguous amino acids;

(h) a fragment of the amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369, wherein the fragment comprises at least 12 contiguous amino acids;

(i) the amino acid sequence of the mature receptor polypeptide from about amino acid 6 to about amino acid 359, shown in SEQ ID NO:1;

(j) the amino acid sequence of the mature polypeptide from about amino acid 6 to about amino acid 359, encoded by the cDNA clone contained in ATCC Deposit No. PTA-2369;

(k) the amino acid sequence of the transmembrane domain of the polypeptide shown in SEQ ID NO:1, from about amino acid 43 to about amino acid 318;

(l) the amino acid sequence of the transmembrane domain from about amino acid 43 to about amino acid 318 in the polypeptide encoded by the cDNA contained in ATCC Deposit No. PTA-2369;

(m) the amino acid sequence of an epitope bearing region of any one of the polypeptides of (a)-(l);]

said method comprising contacting said sample with an agent that specifically allows detection of the presence of the polypeptide in the sample and then detecting the presence of the polypeptide.

18. (Twice Amended) A method for identifying an agent that binds to a polypeptide having an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence shown in SEQ ID NO:1; and

(b) the amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369;

[(c) the amino acid sequence of an allelic variant of the amino acid sequence shown in SEQ ID NO:1;

(d) the amino acid sequence of an allelic variant of the amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369;

(e) the amino acid sequence of a sequence variant of the amino acid sequence shown in SEQ ID NO:1, wherein the sequence variant is encoded by a nucleic acid molecule hybridizing to the nucleic acid molecule shown in SEQ ID NO 2 under stringent conditions;

(f) the amino acid sequence of a sequence variant of the amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. PTA-2369, wherein the sequence variant is encoded by a nucleic acid molecule hybridizing under stringent conditions to the cDNA contained in ATCC Deposit No. PTA-2369;

(g) a fragment of the amino acid sequence shown in SEQ ID NO:1, wherein the fragment comprises at least 12 contiguous amino acids;

(h) a fragment of the amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369, wherein the fragment comprises at least 12 contiguous amino acids;

(i) the amino acid sequence of the mature receptor polypeptide from about amino acid 6 to about amino acid 359, shown in SEQ ID NO:1;

(j) the amino acid sequence of the mature polypeptide from about amino acid 6 to about amino acid 359, encoded by the cDNA clone contained in ATCC Deposit No. PTA-2369;

(k) the amino acid sequence of the transmembrane domain of the polypeptide shown in SEQ ID NO:1, from about amino acid 43 to about amino acid 318;

(l) the amino acid sequence of the transmembrane domain from about amino acid 43 to about amino acid 318 in the polypeptide encoded by the cDNA contained in ATCC Deposit No. PTA-2369;

(m) the amino acid sequence of an epitope bearing region of any one of the polypeptides of (a)-(l);]

said method comprising contacting the polypeptide with an agent that binds to the polypeptide and assaying the complex formed with the agent bound to the polypeptide.

19. (Twice amended) A method for modulating the activity of a polypeptide having an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence shown in SEQ ID NO:1; and

(b) the amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369;

[(c) the amino acid sequence of an allelic variant of the amino acid sequence shown in SEQ ID NO:1;

(d) the amino acid sequence of an allelic variant of the amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369;

(e) the amino acid sequence of a sequence variant of the amino acid sequence shown in SEQ ID NO:1, wherein the sequence variant is encoded by a nucleic acid molecule hybridizing to the nucleic acid molecule shown in SEQ ID NO 2 under stringent conditions;

(f) the amino acid sequence of a sequence variant of the amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. PTA-2369, wherein the sequence variant is encoded by a nucleic acid molecule hybridizing under stringent conditions to the cDNA contained in ATCC Deposit No. PTA-2369;

(g) a fragment of the amino acid sequence shown in SEQ ID NO:1, wherein the fragment comprises at least 12 contiguous amino acids;

(h) a fragment of the amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-2369, wherein the fragment comprises at least 12 contiguous amino acids;

(i) the amino acid sequence of the mature receptor polypeptide from about amino acid 6 to about amino acid 359, shown in SEQ ID NO:1;

(j) the amino acid sequence of the mature polypeptide from about amino acid 6 to about amino acid 359, encoded by the cDNA clone contained in ATCC Deposit No. PTA-2369;

(k) the amino acid sequence of the transmembrane domain of the polypeptide shown in SEQ ID NO:1, from about amino acid 43 to about amino acid 318;

(l) the amino acid sequence of the transmembrane domain from about amino acid 43 to about amino acid 318 in the polypeptide encoded by the cDNA contained in ATCC Deposit No. PTA-2369;

(m) the amino acid sequence of an epitope bearing region of any one of the polypeptides of (a)-(l);]

said method comprising contacting the polypeptide with an agent under conditions that allow the agent to modulate the activity of the polypeptide.